

### AMENDMENTS TO THE CLAIMS:

Please amend the claims as follows:

1-3 (Cancelled)

4. (Currently amended) A method of ErbB4 inhibitor design, comprising:

- (a) generating a three dimensional computer model which represents ErbB4 kinase domain in liganded form, wherein said kinase domain described by the amino acid sequence of SEQ ID NO: 1 and having has the structural coordinates of Table 2;
- (b) evaluating compounds as potential ErbB4 inhibitors using said model; and
- (c) selecting compounds for further testing based on said evaluation; and
- (d) testing the compounds selected in step (c) for their inhibitory effect on ErbB4.

5. (Cancelled) A method of ErbB4 inhibitor design, comprising:

6. (Currently amended) A method of ErbB4 inhibitor design, comprising:

- (a) generating a three dimensional computer model which represents a ErbB4 kinase domain in liganded form, wherein said kinase domain has described by the amino acid sequence of SEQ ID NO: 1 and having the structural coordinates of Table 2;

(b) evaluating compounds as potential ErbB4 inhibitors using said model; wherein said evaluation comprises identifying compounds capable of at least one of the following ErbB4 kinase domain/compound interactions:

- (i) one or more interactions with amino acid residues 796, 797, 798, 799, and 800;
  - (ii) one or more interactions with amino acid residues 724, 749, and 850;
  - (iii) one or more interactions with amino acid residues 848, 860, 803, 847, 732, and 725;
  - (iv) one or more interactions with amino acid residues 732, 749, 751, 796, 861, 860, 772, 781, 783, 794, 796, and 862; and
  - (v) one or more interactions with residues 801, 802, 803, 806, and 810;
- and

- (c) selecting compounds for further testing based on said evaluation; and
- (d) testing the compounds selected in step (c) for their inhibitory effect on ErbB4.

7-9. (Cancelled)

10. (New) The method according to claim 4, wherein said method comprises:

(a) generating a three dimensional computer model which represents a ErbB4 kinase domain in liganded form, wherein said kinase domain has the structural coordinates set forth in Table 2;

(b) evaluating compounds as potential ErbB4 inhibitors using said model; wherein said evaluation comprises identifying compounds capable of one or more hydrogen binding interactions with methionine 799;

(c) selecting compounds for further testing based on said evaluation; and

(d) testing the compounds selected in step (c) for their inhibitory effect on ErbB4.

11. (New) The method according to claim 4, wherein said method comprises:

(a) generating a three dimensional computer model which represents a ErbB4 kinase domain in liganded form, wherein said kinase domain has the structural coordinates set forth in Table 2;

(b) evaluating compounds as potential ErbB4 inhibitors using said model; wherein said evaluation comprises identifying compounds capable of one or more of the following interactions:

(i) a hydrophobic interaction with alanine 749;

(ii) an interaction with leucine 724; and

(iii) an interaction with leucine 850;

(c) selecting compounds for further testing based on said evaluation; and

(d) testing the compounds selected in step (c) for their inhibitory effect on ErbB4.

12. (New) The method according to claim 4, wherein said method comprises:

(a) generating a three dimensional computer model which represents a ErbB4 kinase domain in liganded form, wherein said kinase domain has the structural coordinates set forth in Table 2;

(b) evaluating compounds as potential ErbB4 inhibitors using said model; wherein said evaluation comprises identifying compounds capable of one or more of the following interactions:

(i) an interaction with asparagine 848;

- (ii) an interaction with threonine 860;
- (iii) a covalent interaction with cysteine 803;
- (iv) an interaction with cysteine arginine 847;
- (v) an interaction with valine 732; and
- (vi) an interaction with glycine 725;
- (c) selecting compounds for further testing based on said evaluation; and
- (d) testing the compounds selected in step (c) for their inhibitory effect on ErbB4.

13. (New) The method according to claim 4, wherein said method comprises:

(a) generating a three dimensional computer model which represents a ErbB4 kinase domain in liganded form, wherein said kinase domain has the structural coordinates set forth in Table 2;

(b) evaluating compounds as potential ErbB4 inhibitors using said model; wherein said evaluation comprises identifying compounds capable of one or more of the following interactions:

- (i) a hydrophobic interaction with valine 732;
- (ii) a hydrophobic interaction with alanine 749;
- (iii) a hydrophobic interaction with lysine 751;
- (iv) a hydrophobic interaction with threonine 796;
- (v) a hydrophobic interaction with aspartic acid 861;
- (vi) a hydrophobic interaction with threonine 860;
- (vii) a hydrophobic interaction with methionine 772;
- (viii) a hydrophobic interaction with valine 781;
- (ix) a hydrophobic interaction with leucine 783;
- (x) a hydrophobic interaction with leucine 794;
- (xi) a hydrophobic interaction with threonine 796; and
- (xii) a hydrophobic interaction with phenylalanine 862;
- (c) selecting compounds for further testing based on said evaluation; and
- (d) testing the compounds selected in step (c) for their inhibitory effect on ErbB4.

14. (New) The method according to claim 4, wherein said method comprises:

(a) generating a three dimensional computer model which represents a ErbB4 kinase domain in liganded form, wherein said kinase domain has the structural coordinates set forth in Table 2;

(b) evaluating compounds as potential ErbB4 inhibitors using said model; wherein said evaluation comprises identifying compounds capable of one or more of the following interactions:

(i) an interaction with histidine 801;

(ii) an interaction with glycine 802;

(iii) an interaction with cysteine 803;

(iv) an interaction with glutamic acid 806; and

(v) an interaction with glutamic acid 810;

(c) selecting compounds for further testing based on said evaluation; and

(d) testing the compounds selected in step (c) for their inhibitory effect on

ErbB4.